



GeneStream align Home Page

align Search Help

## align Results

Please site: *Pearson, W.R., Wood, T., Zhang, Z., and Miller, W. (1997)*  
*Comparison of DNA sequences with protein sequences, Genomics 46: 24-36*

```
>_                                     390 aa vs.
>_                                     76 aa
scoring matrix: , gap penalties: -12/-2
7.4% identity;          Global alignment score: -560

      10      20      30      40      50      60
935757 MAVESQLKKMVSKYKYRDLTVRETNVNITLYKDLKPVLD SYVFNDGSSRELMNLTGTIP
      : .
      MQI-----
-

      70      80      90      100     110     120
935757 VPYRGNTYNIPICLWLLDTYPYNPPICFVKPTSSMTIKTGKHVDANGKIYLPYLHEWKHP
      : : : : : :
      -----FVKTL-----TGKTI-----
-                               10

      130     140     150     160     170     180
935757 QSDLLGLIQVMIVVFGDEPPVFSRPISASYPPYQATGPPNTSYMPGMPGGISPYPGYP
-

      190     200     210     220     230     240
935757 NPSGYPGCPYPPGGPYPATSSQYPSQPPVTTVGPSRDGTISED TIRASLISAVSDKLRW
      . : : : : :
      -----TLEVEPS-----DTI-----
-                               20

      250     260     270     280     290     300
935757 RMKEEMDRAQAELNALKRTEEDLKKGHQKLEEMVTRL DQAEVDKNIELLKKKDEELSS
      : : : : : :
      -----ENVKA-----KIQDKEG--
-                               30

      310     320     330     340     350     360
935757 ALEKMENQSENNDIDEVIIPTAPLYKQILNLYAEENAIEDTIFYLGEALRRGVIDLDVFL
      : : : : : :
      -----IP--PDQQRLI-----FAGKQLEDG-----
-                               40                               50
```



370 380 390  
935757 KHVRLLSRKQFQLRALMQKARKTAGLSDLY  
: : : . . . . . :  
---RTLSDYNIQKESTLHLVLRRLRG---G  
60 70

Elapsed time: 0:00:00